Conor R. Walker

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Education

University of Cambridge, UK *2017-Present*
PhD in Computational Biology · expected Q4 2021
- Thesis (submitted): Statistical analysis of short template switch mutations in human genomes
- Advisers: Nick Goldman, Aylwyn Scally
- Committee: Zamin Iqbal, Jan Korbel

Newcastle University, UK *2016-2017*
MSc Bioinformatics · first-class honours (83%)
- Thesis: Optimising nucleic acid sequences for DNA strand displacement systems
- Adviser: Harold Fellermann

Liverpool John Moores University, UK *2013-2016*
BSc (Hons) Zoology · first-class honours (80%)
- Thesis: The genetics of insecticide resistance in the blackfly *Simulium vittatum*
- Advisers: Craig Wilding, Will Swaney

Research experience

EMBL - European Bioinformatics Institute, UK *2017-Present*
Predoctoral Researcher · Adviser: Nick Goldman
- I have developed statistical methods to identify template switch variants in DNA sequences
- I have characterised the human evolutionary, population, and cancer landscape of template switch mutagenesis
- I have designed convolutional neural networks for accurately detecting between-species positive selection, validated through large-scale simulation of training and testing data
- I processed large collections of SARS-CoV-2 sequencing data, from which our group has produced a community resource that is used in ongoing global pandemic phylogenetic analyses

This work was funded by both EMBL and NIHR BRC.

Newcastle University, UK *2016-2017*
Postgraduate Student Research
- I implemented multi-objective genetic algorithms for designing and optimising DNA sequences for use in DNA computing systems

Liverpool John Moores University, UK *2016*
Undergraduate Student Research
- I identified enzyme families and point mutations associated with insecticide resistance in a medically-important blackfly genome using phylogenetic methods

Research Assistant *2014-2016*
- I processed nematode samples from across the UK for sequencing using various molecular biology protocols in a wet lab environment

Publications

Peer-reviewed

Mutation rates and selection on synonymous mutations in SARS-CoV-2.
De Maio N., Walker C. R., Turakhia Y., Lanfear R., Corbett-Detig R., Goldman N.
Genome Biology and Evolution 13, evab087 (2021).

Short-range template switching in great ape genomes explored using pair hidden Markov models.
Walker C. R., Scally A., De Maio N., Goldman N.
PLOS Genetics 17, e1009221 (2021).

Stability of SARS-CoV-2 phylogenies.
Turakhia Y., De Maio N., Thornlow B., Gozashti L., Lanfear R., Walker C. R., Hinrichs A. S., Fernandes J. D., Borges R., Slodkowicz G., Weilguny L., Haussler D., Goldman N., Corbett-Detig R.
PLOS Genetics 16, e1009175 (2020).

A phylodynamic workflow to rapidly gain insights into the dispersal history and dynamics of SARS-CoV-2 lineages.
Dellicour S., Durkin K., Hong S. L., Vanmechelen B., Martí-Carreras J., Gill M. S., Meex C., Bontems S., André E., Gilbert M., Walker C. R., De Maio N., Faria N. R., Hadfield J., Hayette M., Bours V., Wawina-Bokalanga T., Artesi M., Baele G., Maes P.
Molecular Biology and Evolution 38, 1608–1613 (2020).

Preprint/equivalent

phastSim: efficient simulation of sequence evolution for pandemic-scale datasets.
De Maio N., Boulton W., Weilguny L., Walker C. R., Turakhia Y., Corbett-Detig R., Goldman N.
bioRxiv, doi.org/10.1101/2021.03.15.435416 (2021).

Masking strategies for SARS-CoV-2 alignments.
De Maio N., Walker C. R., Borges R., Weilguny L., Slodkowicz G., Goldman N.
virological.org/t/masking-strategies-for-sars-cov-2-alignments/480 (2020).

Issues with SARS-CoV-2 sequencing data.
De Maio N., Walker C. R., Borges R., Weilguny L., Slodkowicz G., Goldman N.
virological.org/t/issues-with-sars-cov-2-sequencing-data/473 (2020).

Selected presentations

ISMB/ECCB 2021	*Jul. 2021*

Talk: Accurate detection of positive selection using convolutional neural networks
Walker C. R., De Maio N., Goldman N.

SMBE 2021	*Jul. 2021*

Talk: Accurate detection of positive selection using convolutional neural networks
Walker C. R., De Maio N., Goldman N.

Evolution 2021	*Jun. 2021*

Talk: Accurate detection of positive selection using convolutional neural networks
Walker C. R., De Maio N., Goldman N.

SMBE 2019	*Jul. 2019*

Poster: Short template switches explain mutation clusters in the human genome
Walker C. R., De Maio N., Goldman N.

EMBL-EBI PhD Seminar Day	*May 2019*

Talk: Short-range template switching in the human genome
Walker C. R.

NIHR BRC Annual Research Day	*Jul. 2018*

Talk: Investigating short template switch mutations in humans and model organisms
Walker C. R.

Phylogroup XI	*Mar. 2018*

Talk: Short template switch events explain mutation clusters in the human genome
Walker C. R., Löytynoja A., Goldman N.

Teaching

Students supervised

Fatma Rabia Fidan   *2021*
- Masters-level project: Identifying *de novo* template switch mutations in trios of human genomes

Shayesteh Arasti (co-advised with Nicola De Maio)   *2021*
- Masters-level project: Using convolutional neural networks to detect positive selection

Viacheslav Vasilev (co-advised with Nicola De Maio)   *2020*
- Masters-level project: Using convolutional neural networks to detect positive selection

William Xu (co-advised with Nicola De Maio)   *2020*
- Masters-level project: Using convolutional neural networks to detect positive selection

Teaching assistant

Medics to Coders · University of Cambridge, UK   *2018*
- I helped to deliver practical sessions on programming in Python at the School of Clinical Medicine

Honours and awards

Best student talk   *May 2019*
- Audience vote at the annual EMBL-EBI PhD Seminar Day

Outstanding performance by a MSc Bioinformatics programme student   *Oct. 2017*
- Awarded for achieving the highest overall grade on my master's degree programme

Zoology prize   *Sep. 2016*
- Awarded for achieving the highest overall grade on my bachelor's degree programme

Other scientific activities

Committees

Student Representative · EMBL-EBI, UK   *2018-2020*
- Attended meetings with senior management from across all EMBL outstations to discuss issues impacting the graduate community at EMBL
- Organised a variety of academic and social events within the institution

Graduate Student and Post-Doc Forum member · University of Cambridge, UK   *2018*
- I worked as part of a group of students and postdocs to devise strategies for creating a more positive experience for graduate students in the School of Life Sciences

Memberships

International Society for Computational Biology
Society for Molecular Biology and Evolution
Society for the Study of Evolution

Reviewer for

Nature Medicine
Molecular Biology and Evolution
BMC Bioinformatics

Skills

Programming	Python, Bash, C++, R, AWK, LaTeX
Libraries	Numpy, SciPy, Keras, TensorFlow, PyTorch, scikit-allel, matplotlib, seaborn
Coding practices	Git, Snakemake, unit testing, Docker, Singularity, Jupyter, Vim
High performance computing	Daily use of both CPU and GPU clusters in a LSF environment
Operating systems	Linux, MacOS